

## RAW SEQUENCE LISTING

The Biotechnology Systems Branch of the Scientific and Technical  
Information Center (STIC) no errors detected.

Application Serial Number:

09/277401 B

Source:

FW16

Date Processed by STIC:

5/9/5

# ***ENTERED***



IFW16

## RAW SEQUENCE LISTING

DATE: 05/09/2005

PATENT APPLICATION: US/09/277,401B

TIME: 16:40:23

Input Set : A:\PTO.FG.txt

Output Set: N:\CRF4\05092005\I277401B.raw

## SEQUENCE LISTING

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3 (1) GENERAL INFORMATION:
C--> 4 (i) APPLICANT: Jaye, Michael C.
5      Lynch, Kevin J.
6      Amin, Dilip V.
7      Doan, Kim Anh T.
8      Marchadier, Dawn
9      Maugeais, Cyrille
10     Rader, Daniel J.
11     Krawiec, John A.
12     South, Victoria J.
13     (ii) TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR EFFECTING THE LEVELS OF
14     HIGH DENSITY LIPOPROTEIN (HDL) CHOLESTEROL AND
APOLIPOPROTEIN AI, VERY LOW
15     DENSITY LIPOPROTEIN (VLDL) CHOLESTEROL AND LOW DENSITY
LIPOPROTEIN (LDL)
16     (iii) NUMBER OF SEQUENCES: 27
17     (iv) CORRESPONDENCE ADDRESS:
18         (A) ADDRESSEE: Synnestvedt & Lechner LLP
19         (B) STREET: Suite 2600 Aramark Tower, 1101 Market Street
20         (C) CITY: Philadelphia
21         (D) STATE: PA
22         (E) COUNTRY: USA
23         (F) ZIP: 19107
24     (v) COMPUTER READABLE FORM:
25         (A) MEDIUM TYPE: Floppy disk
26         (B) COMPUTER: IBM PC compatible
27         (C) OPERATING SYSTEM: PC Windows 95
28         (D) SOFTWARE: Microsoft Word converted to ASCII
29     (vi) CURRENT APPLICATION DATA:
C--> 30         (A) APPLICATION NUMBER: US/09/277,401B
C--> 31         (B) FILING DATE: 26-Mar-1999
32         (C) CLASSIFICATION:
33     (viii) ATTORNEY/AGENT INFORMATION:
34         (A) NAME: Yao, Gene J.
35         (B) REGISTRATION NUMBER: 47,193
36         (C) REFERENCE/DOCKET NUMBER: 22,944 C USA
37     (ix) TELECOMMUNICATION INFORMATION:
38         (A) TELEPHONE: (215) 923 4466
39         (B) TELEFAX: (215) 923 2189
41 (2) INFORMATION FOR SEQ ID NO: 1:
42     (i) SEQUENCE CHARACTERISTICS:
43         (A) LENGTH: 367 base pairs
44         (B) TYPE: nucleic acid

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45

(C) STRANDEDNESS: double

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46      (D) TOPOLOGY: linear
47      (ii) MOLECULE TYPE: cDNA
48      (ix) FEATURE:
49          (A) NAME/KEY: CDS
50          (B) LOCATION: 22..180
51      (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 1:
52 GAATTCGGCT TGATCAATCG C TTC AAA AAG GGG ATC TGT CTG AGC TGC CGC      51
53      Phe Lys Lys Gly Ile Cys Leu Ser Cys Arg
54      1 5 10
56 AAG AAC CGT TGT AAT AGC ATT GGC TAC AAT GCC AAG AAA ATG AGG AAC      99
57 Lys Asn Arg Cys Asn Ser Ile Gly Tyr Asn Ala Lys Lys Met Arg Asn
58      15 20 25
60 AAG AGG AAC AGC AAA ATG TAC CTA AAA ACC CGG GCA GGC ATG CCT TTC      147
61 Lys Arg Asn Ser Lys Met Tyr Leu Lys Thr Arg Ala Gly Met Pro Phe
62      30 35 40
63 AGA GGT AAC CTT CAG TCC CTG GAG TGT CCC TGA GGAAGGCCCT TAATACCTCC      200
64 Arg Gly Asn Leu Gln Ser Leu Glu Cys Pro
65      45 50
66 TTCTTAATAC CATGCTGCAG AGCAGGGCAC ATCCTAGCCC AGGAGAAGTG GCCAGCACAA      260
67 TCCAATCAAA TCGTTGCAAA TCAGATTACA CTGTGCATGT CCTAGGAAAG GGAATCTTTA      320
68 CAAATAAAC AGTGTGGACC CCTCAAAAAA AAAAAAAGC CGAATTC      367
70 (2) INFORMATION FOR SEQ ID NO: 2:
71      (i) SEQUENCE CHARACTERISTICS:
72          (A) LENGTH: 52 amino acids
73          (B) TYPE: amino acid
74          (D) TOPOLOGY: linear
75      (ii) MOLECULE TYPE: protein
76      (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 2:
77 Phe Lys Lys Gly Ile Cys Leu Ser Cys Arg Lys Asn Arg Cys Asn Ser
78 1 5 10 15
79 Ile Gly Tyr Asn Ala Lys Lys Met Arg Asn Lys Arg Asn Ser Lys Met
80 20 25 30
81 Tyr Leu Lys Thr Arg Ala Gly Met Pro Phe Arg Gly Asn Leu Gln Ser
82 35 40 45
83 Leu Glu Cys Pro
84 50
86 (2) INFORMATION FOR SEQ ID NO: 3:
87      (i) SEQUENCE CHARACTERISTICS:
88          (A) LENGTH: 1382 base pairs
89          (B) TYPE: nucleic acid
90          (C) STRANDEDNESS: double
91          (D) TOPOLOGY: linear
92      (ii) MOLECULE TYPE: cDNA
93      (ix) FEATURE:
94          (A) NAME/KEY: CDS
95          (B) LOCATION: 312..1370
96      (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 3:
97 GAATTCGGCT TCTACTACTA CTAGGCCACG CGTCGCCTAG TACGGGGGGG GGGGGGGGGG      60
98 TCAGCGAGTC CTTGCCTCCC GCGGGCTCAG GACGAGGGCA GATCTCGTTC TGGGGCAAGC      120

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99	CGTTGACACT	CGCTCCCTGC	CACCGCCCGG	GCTCCGTGCC	GCCAAGTTTT	CATTTTCCAC	180
100	CTTCTCTGCC	TCCAGTCCCC	CAGCCCCTGG	CCGAGAGAAG	GGTCTTACCG	GCCGGGATTG	240
101	CTGGAAACAC	CAAGAGGTGG	TTTTTGTTTT	TTAAAACTTC	TGTTTCTTGG	GAGGGGGTGT	300
102	GGCGGGGCAG	G	ATG	AGC	AAC	TCC	350
103		Met	Ser	Asn	Ser	Val	
104		1		5		10	
105	TGC	TAT	TGC	TTT	GCT	GCG	398
106	Cys	Tyr	Cys	Phe	Ala	Ala	
107	15			20		25	
108	CGG	CTG	GAA	GAT	AAG	CTC	446
109	Arg	Leu	Glu	Asp	Lys	Leu	
110	30			35		40	45
111	AAA	CCA	TCT	GTG	AGG	TTT	494
112	Lys	Pro	Ser	Val	Arg	Phe	
113				50		55	60
114	GAA	GGA	TGC	TAC	CTC	TCC	542
115	Glu	Gly	Cys	Tyr	Leu	Ser	
116				65		70	75
117	AGT	TTC	AAC	ATG	ACA	GCT	590
118	Ser	Phe	Asn	Met	Thr	Ala	
119	80			85		90	
120	ATG	AGC	GGT	ATC	TTT	GAA	638
121	Met	Ser	Gly	Ile	Phe	Glu	
122	95			100		105	
123	CAC	ACA	AGA	GAG	AAA	GAC	686
124	His	Thr	Arg	Glu	Lys	Asp	
125	110			115		120	125
126	CTG	GCC	CAC	CAG	CTT	TAC	734
127	Leu	Ala	His	Gln	Leu	Tyr	
128				130		135	140
129	GGA	CAC	AGC	ATT	GCC	AGG	782
130	Gly	His	Ser	Ile	Ala	Arg	
131				145		150	155
132	TTT	TCT	CTC	GGG	AAT	GTC	830
133	Phe	Ser	Leu	Gly	Asn	Val	
134	160			165		170	
135	GTG	GCC	GGG	TAT	GCA	GGC	878
136	Val	Ala	Gly	Tyr	Ala	Gly	
137	175			180		185	
138	ACA	GGT	TTG	GAT	CCT	GCC	926
139	Thr	Gly	Leu	Asp	Pro	Ala	
140	190			195		200	205
141	AAG	AGG	CTC	TCT	CCG	GAC	974
142	Lys	Arg	Leu	Ser	Pro	Asp	
143				210		215	220
144	TAC	ACG	CGT	TCC	TTC	GGC	1022
145	Tyr	Thr	Arg	Ser	Phe	Gly	
146				225		230	235
147	CAC	ATT	GAC	ATC	TAC	CCC	1070

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148 His Ile Asp Ile Tyr Pro Asn Gly Gly Asp Phe Gln Pro Gly Cys Gly
149      240      245      250
150 CTC AAC GAT GTC TTG GGA TCA ATT GCA TAT GGA ACA ATC ACA GAG GTG      1118
151 Leu Asn Asp Val Leu Gly Ser Ile Ala Tyr Gly Thr Ile Thr Glu Val
152      255      260      265
153 GTA AAA TGT GAG CAT GAG CGA GCC GTC CAC CTC TTT GTT GAC TCT CTG      1166
154 Val Lys Cys Glu His Glu Arg Ala Val His Leu Phe Val Asp Ser Leu
155 270      275      280      285
156 GTG AAT CAG GAC AAG CCG AGT TTT GCC TTC CAG TGC ACT GAC TCC AAT      1214
157 Val Asn Gln Asp Lys Pro Ser Phe Ala Phe Gln Cys Thr Asp Ser Asn
158      290      295      300
159 CGC TTC AAA AAG GGG ATC TGT CTG AGC TGC CGC AAG AAC CGT TGT AAT      1262
160 Arg Phe Lys Lys Gly Ile Cys Leu Ser Cys Arg Lys Asn Arg Cys Asn
161      305      310      315
162 AGC ATT GGC TAC AAT GCC AAG AAA ATG AGG AAC AAG AGG AAC AGC AAA      1310
163 Ser Ile Gly Tyr Asn Ala Lys Lys Met Arg Asn Lys Arg Asn Ser Lys
164      320      325      330
165 ATG TAC CTA AAA ACC CGG GCA GGC ATG CCT TTC AGA GGT AAC CTT CAG      1358
166 Met Tyr Leu Lys Thr Arg Ala Gly Met Pro Phe Arg Gly Asn Leu Gln
167      335      340      345
168 TCC CTG GAG TGT CAAGCCGAAT TC      1382
169 Ser Leu Glu Cys
170 350
172 (2) INFORMATION FOR SEQ ID NO: 4:
173     (i) SEQUENCE CHARACTERISTICS:
174         (A) LENGTH: 353 amino acids
175         (B) TYPE: amino acid
176         (D) TOPOLOGY: linear
177     (ii) MOLECULE TYPE: protein
178     (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 4:
180 Met Ser Asn Ser Val Pro Leu Leu Cys Phe Trp Ser Leu Cys Tyr Cys
181 1      5      10      15
182 Phe Ala Ala Gly Ser Pro Val Pro Phe Gly Pro Glu Gly Arg Leu Glu
183      20      25      30
184 Asp Lys Leu His Lys Pro Lys Ala Thr Gln Thr Glu Val Lys Pro Ser
185      35      40      45
186 Val Arg Phe Asn Leu Arg Thr Ser Lys Asp Pro Glu His Glu Gly Cys
187      50      55      60
188 Tyr Leu Ser Val Gly His Ser Gln Pro Leu Glu Asp Cys Ser Phe Asn
189 65      70      75      80
190 Met Thr Ala Lys Thr Phe Phe Ile Ile His Gly Trp Thr Met Ser Gly
191      85      90      95
192 Ile Phe Glu Asn Trp Leu His Lys Leu Val Ser Ala Leu His Thr Arg
193      100      105      110
194 Glu Lys Asp Ala Asn Val Val Val Val Asp Trp Leu Pro Leu Ala His
195      115      120      125
196 Gln Leu Tyr Thr Asp Ala Val Asn Asn Thr Arg Val Val Gly His Ser
197      130      135      140
198 Ile Ala Arg Met Leu Asp Trp Leu Gln Glu Lys Asp Asp Phe Ser Leu

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199 145          150          155          160
200 Gly Asn Val His Leu Ile Gly Tyr Ser Leu Gly Ala His Val Ala Gly
201          165          170          175
202 Tyr Ala Gly Asn Phe Val Lys Gly Thr Val Gly Arg Ile Thr Gly Leu
203          180          185          190
204 Asp Pro Ala Gly Pro Met Phe Glu Gly Ala Asp Ile His Lys Arg Leu
205          195          200          205
206 Ser Pro Asp Asp Ala Asp Phe Val Asp Val Leu His Thr Tyr Thr Arg
207          210          215          220
208 Ser Phe Gly Leu Ser Ile Gly Ile Gln Met Pro Val Gly His Ile Asp
209 225          230          235          240
210 Ile Tyr Pro Asn Gly Gly Asp Phe Gln Pro Gly Cys Gly Leu Asn Asp
211          245          250          255
212 Val Leu Gly Ser Ile Ala Tyr Gly Thr Ile Thr Glu Val Val Lys Cys
213          260          265          270
214 Glu His Glu Arg Ala Val His Leu Phe Val Asp Ser Leu Val Asn Gln
215          275          280          285
216 Asp Lys Pro Ser Phe Ala Phe Gln Cys Thr Asp Ser Asn Arg Phe Lys
217          290          295          300
218 Lys Gly Ile Cys Leu Ser Cys Arg Lys Asn Arg Cys Asn Ser Ile Gly
219 305          310          315          320
220 Tyr Asn Ala Lys Lys Met Arg Asn Lys Arg Asn Ser Lys Met Tyr Leu
221          325          330          335
222 Lys Thr Arg Ala Gly Met Pro Phe Arg Gly Asn Leu Gln Ser Leu Glu
223          340          345          350
224 Cys
227 (2) INFORMATION FOR SEQ ID NO: 5:
228     (i) SEQUENCE CHARACTERISTICS:
229         (A) LENGTH: 2565 base pairs
230         (B) TYPE: nucleic acid
231         (C) STRANDEDNESS: double
232         (D) TOPOLOGY: linear
233     (ii) MOLECULE TYPE: cDNA
234     (ix) FEATURE:
235         (A) NAME/KEY: CDS
236         (B) LOCATION: 252..1754
237     (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 5:
238 GAATTCGCGG CCGCGTCGAC GCGGCTCAG GACGAGGGCA GATCTCGTTC TGGGGCAAGC      60
239 CGTTGACACT CGCTCCCTGC CACCGCCCGG GCTCCGTGCC GCCAAGTTTT CATTTTCCAC      120
240 CTTCTCTGCC TCCAGTCCCC CAGCCCCTGG CCGAGAGAAG GGTCTTACCG GCCGGGATTG      180
241 CTGGAACAC CAAGAGGTGG TTTTGTGTTT TTAAACTTC TGTTCCTGG GAGGGGTGT      240
242 GCGGGGCAG G ATG AGC AAC TCC GTT CCT CTG CTC TGT TTC TGG AGC CTC      290
243 Met Ser Asn Ser Val Pro Leu Leu Cys Phe Trp Ser Leu
244          1          5          10
245 TGC TAT TGC TTT GCT GCG GGG AGC CCC GTA CCT TTT GGT CCA GAG GGA      338
246 Cys Tyr Cys Phe Ala Ala Gly Ser Pro Val Pro Phe Gly Pro Glu Gly
247          15          20          25
248 CGG CTG GAA GAT AAG CTC CAC AAA CCC AAA GCT ACA CAG ACT GAG GTC      386
249 Arg Leu Glu Asp Lys Leu His Lys Pro Lys Ala Thr Gln Thr Glu Val

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**VERIFICATION SUMMARY**

DATE: 05/09/2005

PATENT APPLICATION: US/09/277,401B

TIME: 16:40:24

Input Set : A:\PTO.FG.txt

Output Set: N:\CRF4\05092005\I277401B.raw

L:4 M:220 C: Keyword misspelled or invalid format, [(i) APPLICANT:]  
L:30 M:220 C: Keyword misspelled or invalid format, [(A) APPLICATION NUMBER:]  
L:31 M:220 C: Keyword misspelled or invalid format, [(B) FILING DATE:]